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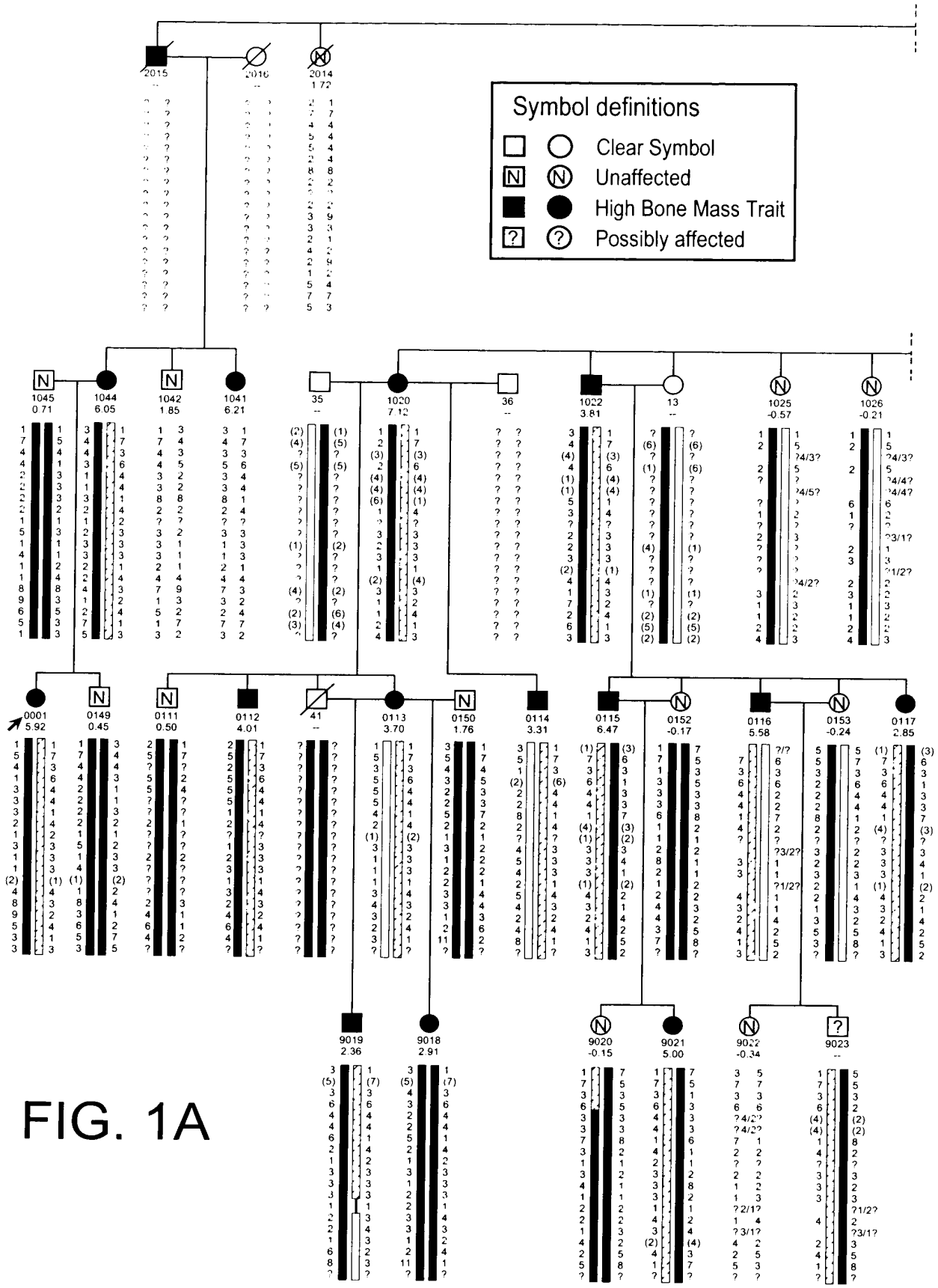

FIG. 1A

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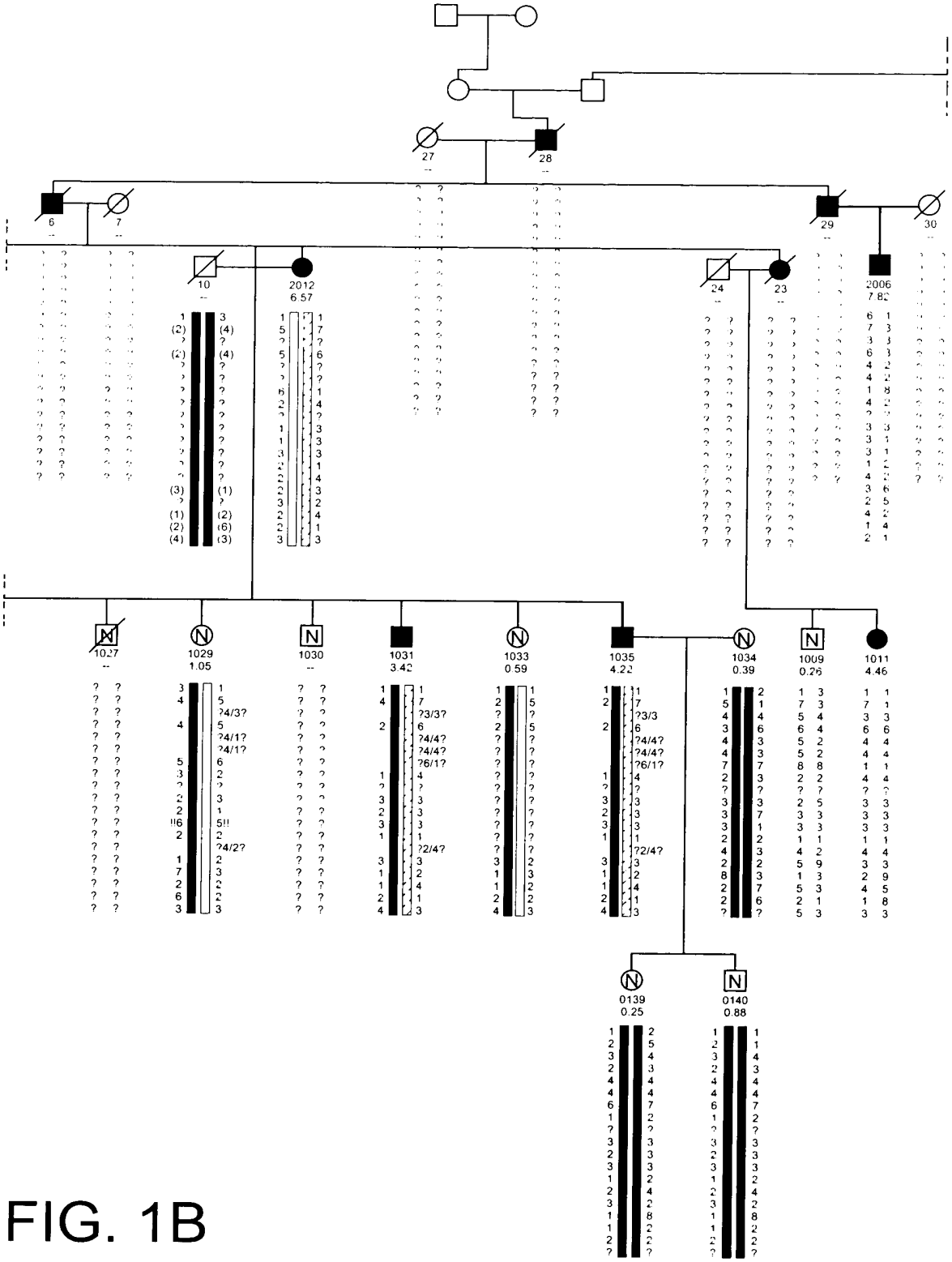

FIG. 1B

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FIG. 2A

BAC/STS Map of the HBM Region

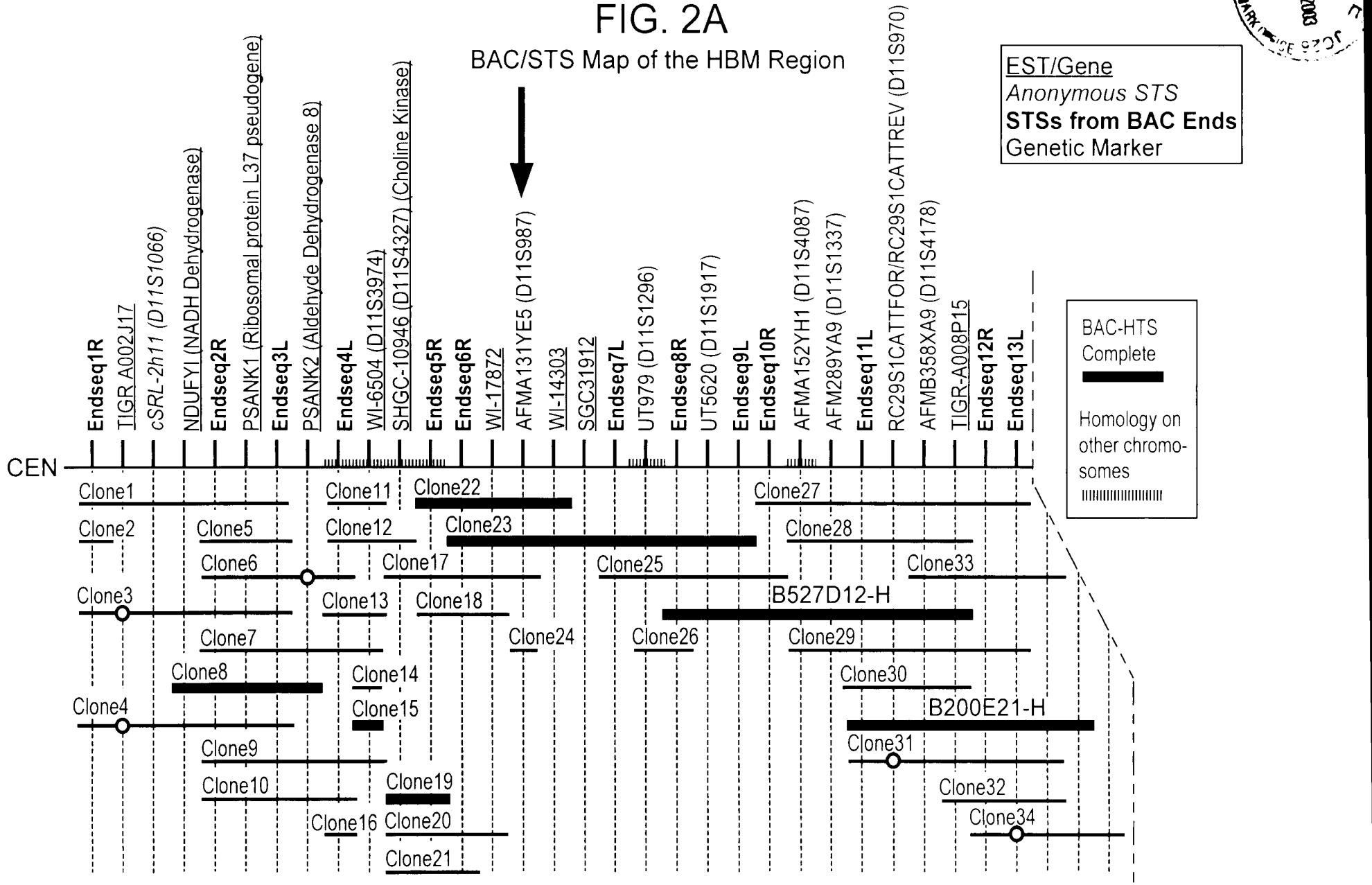
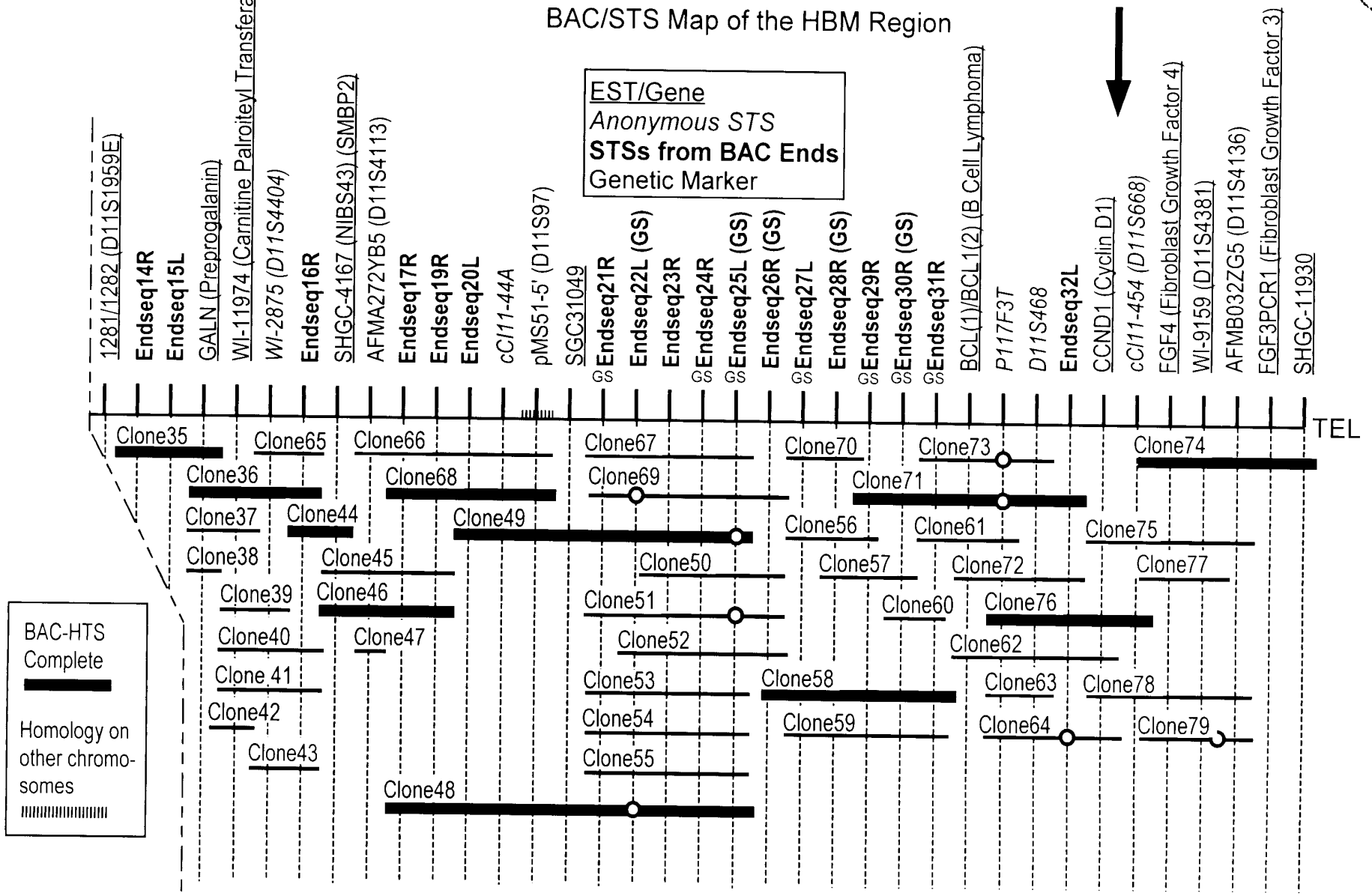


FIG. 2B

BAC/STS Map of the HBM Region



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Exon 1
ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCG
GGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCGCCGCCCGGGCCG
CCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC
TGCCCGGCCCCCGCCGCGGCC

Exon 2 Coordinates: 527d12_Contig308G 30944-30549
gccccacag**CCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGC**
TGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGC
GGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGC
CGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCT
GAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGG
TCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACT
GGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGC
ACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCC
ATCGCCTTGGACCCCGCTCACGGgtaaaccctgctg

... 9408 nt ...

Exon 3 Coordinates: 527d12_Contig308G 21141-20945
ccccgtcacag**GTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTG**
AGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCG
GACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG
CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG
GACGGCTCGTTCCGgtaggtacccac

... 6094 nt ...

Exon 4 Coordinates: 527d12_Contig308G 15047-14850
tccctgactgcag**GCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCC**
CTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGC
TCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGAT
CCTGAGTGCCCTATACTCACCCATGGACATCCAGGTGCTGAGCCAGGA
GCGGCAGCCTTTCTgtgagtgccgg

... 1827 nt ...

Exon 5 Coordinates: 527d12_Contig308G 13220-13088
tttctcag**TCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTG**
TGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACG
GGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGgtgaggcggtgg
gacg

FIG. 3A

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... 20923 nt ...

Exon 6 Coordinates: 527d12_Contig309G 7705-8100
ctccacag**GAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTAC**
GGAGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAGG
TGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGG
GCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCG
TACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAA
CGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTG
GACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCA
CCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCC
ATCGCACTGCACCCCGTGATGGGgtaagacgggc

..... 3211 nt .....

Exon 7 Coordinates: 527d12_Contig309G 11311-11482
ttcttctccag**CCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGA**
GTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTC
CCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGC
TCTACTGGGGAGACGCCAAGACAGACAAGATCGAGgtgaggctcctgtgg

..... 13445 nt .....

Exon 8 Coordinates: 527d12_Contig309G 24927-25143
ccgtcctgcag**GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGA**
GGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCAT
CTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGG
TCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGG
GGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGgtgagtccgggggggtc

....2826 nt .....

Exon 9 Coordinates: 527d12_Contig309G 27969-28256
gttcgcttccag**GAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCA**
CCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGG
CCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTT
CTTGGTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGAC
CAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTC
AGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGT
CAGCCTGAAGgtagcgtgggc

.....3102.....

FIG. 3B

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Exon 10 Coordinates: 527d12_Contig309G 31358-31582
cctgctgccag**ACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCA**
CGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTG
GATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGA
AGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGG
ACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGgtaagtgtt
tgcctgtc

.....1297 nt.....

Exon 11 Coordinates: 527d12_Contig309G 32879-33064
gtgccttccag**CTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCG**
TGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAG
GTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTC
TACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTG
Ggtgagggccgggct

.....2069 nt.....

Exon 12 Coordinates: 527d12_Contig309G 35133-35454
gtgttcatgcag**GTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG**
TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAAT
CTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCAC
CCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCA
CTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCA
GTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCT
GCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCgtaag
tgcctcatggt

.....2006 nt.....

Exon 13 Coordinates: 527d12_Contig309G 37460-37659
gcctcctcta**CGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG**
TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCT
GCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAA
GTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGA
CGACGGGACCCAGgcaggtgccctgtgg

.....6965 nt.....

FIG. 3C

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Exon 14 Coordinates: 527d12_Contig309G 44624-44832
ctttgtcttacag**CCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGAC**
AGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTC
TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGG
GGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGG
CCATCGTCGTCAACGCGGAGCGAGGgtaggaggccaac

……1404 nt…..

Exon 15 Coordinates: 527d12_Contig309G 46236-46427
ccaccctcccgcag**GTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAA**
GATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCA
CCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGG
GCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGT
GACCTGTCAGgtacgcgccccgg

…..686 nt…..

Exon 16 Coordinates: 527d12_Contig309G 47113-47322
ggctgcttgcag**GGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCA**
GCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCG
CCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGC
GGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAG
TGGAGGAAGTCAGCCTGGAGGAGTTCTgtacgtgggggc

…..3884 nt……

Exon 17 Coordinates: 527d12_Contig309G 51206-51331
ttgtctttgcag**CAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACA**
TCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCC
ACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGgtaggtgtgacctaggtgc

….3905 nt…….

Exon 18 Coordinates: 527d12_Contig309G 55236-55472
gttctcctctgtccctccccagg**AGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGT**
GCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGG
CTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGT
GCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGC
GCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAG
GTGGACTGTGACGgtgaggccctcc

…….3052 nt…..

FIG. 3D

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Exon 19 Coordinates: 527d12_Contig309G 58524-58634
tctccttgcag**CCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGT**
GTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACG
GCTCCGACGAGCTCATGTGTGgtgagccagctt

.....1448 nt.....

Exon 20 Coordinates: 527d12_Contig309G 60082-60319
gtttgtctctggcag**AAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACA**
GCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCAT
GGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGC
GGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGC
ACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCT
TCACAGgtaaggagcctgagatatggaa

....1095 nt.....

Exon 21 Coordinates: 527d12_Contig309G 61414-61552
cttccctgccag**GCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTG**
ATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCAC
AGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCC
GCCGgtgaggggcggg

.....6513 nt.....

Exon 22 Coordinates: 527d12_Contig309G 68065-68162
ttggctctcctcag**ATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCC**
TGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGA
GACCGTACAGgtaggacatccccctgcag

.....2273 nt.....

FIG. 3E

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Exon 23 Coordinates: 527d12_Contig309G 70435-70901

tcaaacattccggccactgcgagaccgtacag**GCCCTACATCATTCGAGGAATGGCGCCCC**
CGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCC
AGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCA
GACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCG
GAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCAT
CTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGC
CGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAA
AGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAA
AAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTT
TGTACAGTGGAGAAATATTTATAAACTTAATTTTGTAAAACA

FIG. 3F

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Model for a LDL Receptor-Related protein, Zmax1

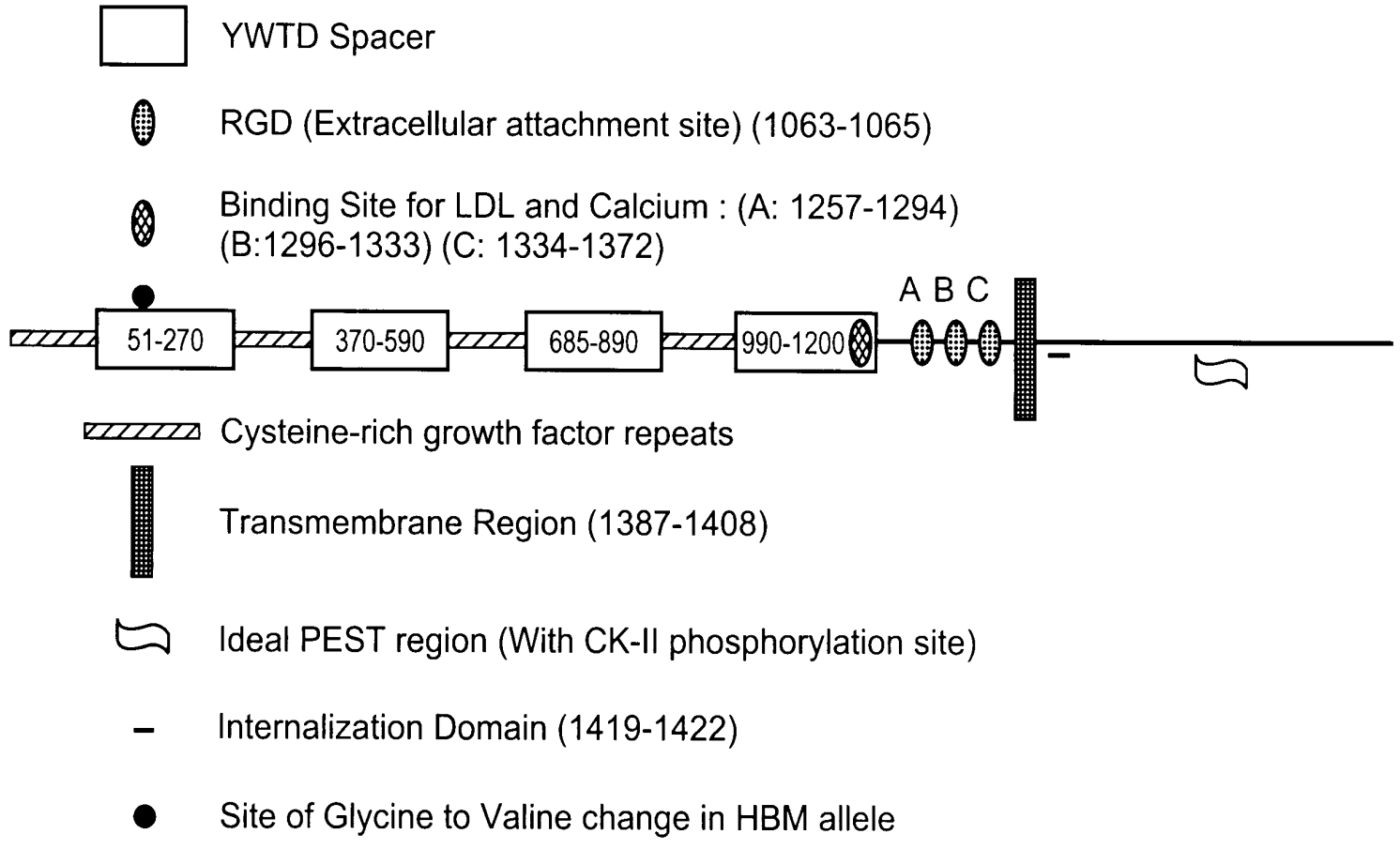

FIG. 4

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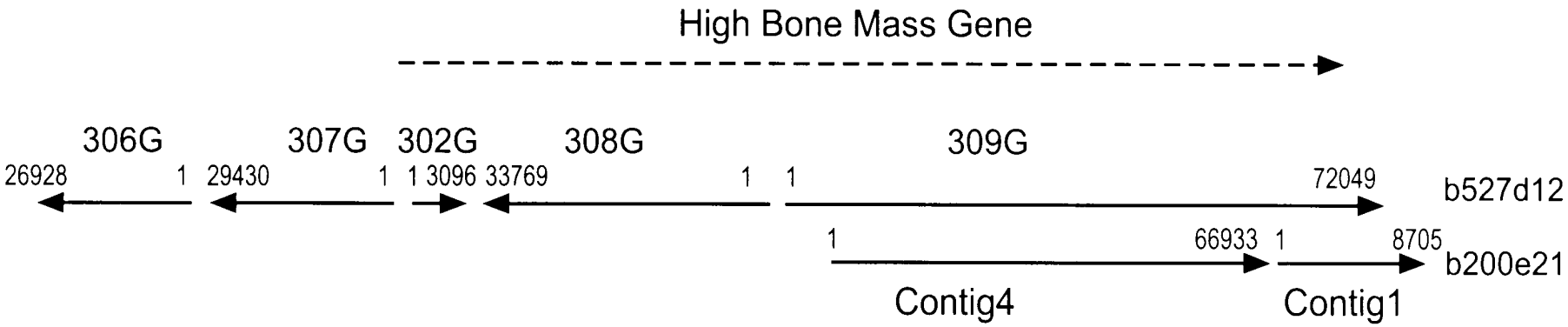

FIG. 5

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FIG. 6A

```
  1  ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC   60
 61  GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT  120
  1            M  E  A  A  P  P  G  P  P  W  P  L  L  L  L  L  L    17

121  GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT  180
 18   L  L  L  A  L  C  G  C  P  A  P  A  A  A  S  P  L  L  L  F   37

181  TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT  240
 38   A  N  R  R  D  V  R  L  V  D  A  G  G  V  K  L  E  S  T  I   57

241  CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT  300
 58   V  V  S  G  L  E  D  A  A  A  V  D  F  Q  F  S  K  G  A  V   77

301  GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC  360
 78   Y  W  T  D  V  S  E  E  A  I  K  Q  T  Y  L  N  Q  T  G  A   97

361  CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG  420
 98   A  V  Q  N  V  V  I  S  G  L  V  S  P  D  G  L  A  C  D  W  117

421  GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT  480
118   V  G  K  K  L  Y  W  T  D  S  E  T  N  R  I  E  V  A  N  L  137

481  CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC  540
138   N  G  T  S  R  K  V  L  F  W  Q  D  L  D  Q  P  R  A  I  A  157

541  CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA  600
158   L  D  P  A  H  G  Y  M  Y  W  T  D  W  G  E  T  P  R  I  E  177
```

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FIG. 6B

```
601  GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC  660
178   R  A  G  M  D  G  S  T  R  K  I  I  V  D  S  D  I  Y  W  P   197

661  CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG  720
198   N  G  L  T  I  D  L  E  E  Q  K  L  Y  W  A  D  A  K  L  S   217

721  CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT  780
218   F  I  H  R  A  N  L  D  G  S  F  R  Q  K  V  V  E  G  S  L   237

781  GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC  840
238   T  H  P  F  A  L  T  L  S  G  D  T  L  Y  W  T  D  W  Q  T   257

841  CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC  900
258   R  S  I  H  A  C  N  K  R  T  G  G  K  R  K  E  I  L  S  A   277

901  CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC  960
278   L  Y  S  P  M  D  I  Q  V  L  S  Q  E  R  Q  P  F  F  H  T   297

961  TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC  1020
298   R  C  E  E  D  N  G  G  C  S  H  L  C  L  L  S  P  S  E  P   317

1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA  1080
318   F  Y  T  C  A  C  P  T  G  V  Q  L  Q  D  N  G  R  T  C  K   337

1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT  1140
338   A  G  A  E  E  V  L  L  L  A  R  R  T  D  L  R  R  I  S  L   357
```

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FIG. 6C

```
1141  GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC  1200
 358   D  T  P  D  F  T  D  I  V  L  Q  V  D  D  I  R  H  A  I  A   377

1201  CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT  1260
 378   I  D  Y  D  P  L  E  G  Y  V  Y  W  T  D  D  E  V  R  A  I   397

1261  CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA  1320
 398   R  R  A  Y  L  D  G  S  G  A  Q  T  L  V  N  T  E  I  N  D   417

1321  CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC  1380
 418   P  D  G  I  A  V  D  W  V  A  R  N  L  Y  W  T  D  T  G  T   437

1381  GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA  1440
 438   D  R  I  E  V  T  R  L  N  G  T  S  R  K  I  L  V  S  E  D   457

1441  CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA  1500
 458   L  D  E  P  R  A  I  A  L  H  P  V  M  G  L  M  Y  W  T  D   477

1501  CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT  1560
 478   W  G  E  N  P  K  I  E  C  A  N  L  D  G  Q  E  R  R  V  L   497

1561  GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT  1620
 498   V  N  A  S  L  G  W  P  N  G  L  A  L  D  L  Q  E  G  K  L   517

1621  CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG  1680
 518   Y  W  G  D  A  K  T  D  K  I  E  V  I  N  V  D  G  T  K  R   537
```

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FIG. 6D

```
1681  GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT  1740
 538   R  T  L  L  E  D  K  L  P  H  I  F  G  F  T  L  L  G  D  F   557

1741  CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG  1800
 558   I  Y  W  T  D  W  Q  R  R  S  I  E  R  V  H  K  V  K  A  S   577

1801  CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC  1860
 578   R  D  V  I  I  D  Q  L  P  D  L  M  G  L  K  A  V  N  V  A   597

1861  CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT  1920
 598   K  V  V  G  T  N  P  C  A  D  R  N  G  G  C  S  H  L  C  F   617

1921  CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT  1980
 618   F  T  P  H  A  T  R  C  G  C  P  I  G  L  E  L  L  S  D  M   637

1981  GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG  2040
 638   K  T  C  I  V  P  E  A  F  L  V  F  T  S  R  A  A  I  H  R   657

2041  GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC  2100
 658   I  S  L  E  T  N  N  N  D  V  A  I  P  L  T  G  V  K  E  A   677

2101  CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA  2160
 678   S  A  L  D  F  D  V  S  N  N  H  I  Y  W  T  D  V  S  L  K   697

2161  GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT  2220
 698   T  I  S  R  A  F  M  N  G  S  S  V  E  H  V  V  E  F  G  L   717
```

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FIG. 6E

```
2221  TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC  2280
 718   D  Y  P  E  G  M  A  V  D  W  M  G  K  N  L  Y  W  A  D  T   737

2281  TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG  2340
 738   G  T  N  R  I  E  V  A  R  L  D  G  Q  F  R  Q  V  L  V  W   757

2341  GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG  2400
 758   R  D  L  D  N  P  R  S  L  A  L  D  P  T  K  G  Y  I  Y  W   777

2401  GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT  2460
 778   T  E  W  G  G  K  P  R  I  V  R  A  F  M  D  G  T  N  C  M   797

2461  GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG  2520
 798   T  L  V  D  K  V  G  R  A  N  D  L  T  I  D  Y  A  D  Q  R   817

2521  CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA  2580
 818   L  Y  W  T  D  L  D  T  N  M  I  E  S  S  N  M  L  G  Q  E   837

2581  GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA  2640
 838   R  V  V  I  A  D  D  L  P  H  P  F  G  L  T  Q  Y  S  D  Y   857

2641  TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG  2700
 858   I  Y  W  T  D  W  N  L  H  S  I  E  R  A  D  K  T  S  G  R   877

2701  GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC  2760
 878   N  R  T  L  I  Q  G  H  L  D  F  V  M  D  I  L  V  F  H  S   897
```

FIG. 6F

```
2761  CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG   2820
 898   S  R  Q  D  G  L  N  D  C  M  H  N  N  G  Q  C  G  Q  L  C    917

2821  CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG   2880
 918   L  A  I  P  G  G  H  R  C  G  C  A  S  H  Y  T  L  D  P  S    937

2881  CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG   2940
 938   S  R  N  C  S  P  P  T  T  F  L  L  F  S  Q  K  S  A  I  S    957

2941  TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG   3000
 958   R  M  I  P  D  D  Q  H  S  P  D  L  I  L  P  L  H  G  L  R    977

3001  GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG   3060
 978   N  V  K  A  I  D  Y  D  P  L  D  K  F  I  Y  W  V  D  G  R    997

3061  CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG   3120
 998   Q  N  I  K  R  A  K  D  D  G  T  Q  P  F  V  L  T  S  L  S   1017

3121  CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC   3180
1018   Q  G  Q  N  P  D  R  Q  P  H  D  L  S  I  D  I  Y  S  R  T   1037

3181  ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC   3240
1038   L  F  W  T  C  E  A  T  N  T  I  N  V  H  R  L  S  G  E  A   1057

3241  CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA   3300
1058   M  G  V  V  L  R  G  D  R  D  K  P  R  A  I  V  V  N  A  E   1077
```

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FIG. 6G

```
3301  GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC   3360
1078   R  G  Y  L  Y  F  T  N  M  Q  D  R  A  A  K  I  E  R  A  A    1097

3361  CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT   3420
1098   L  D  G  T  E  R  E  V  L  F  T  T  G  L  I  R  P  V  A  L    1117

3421  GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA   3480
1118   V  V  D  N  T  L  G  K  L  F  W  V  D  A  D  L  K  R  I  E    1137

3481  GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC   3540
1138   S  C  D  L  S  G  A  N  R  L  T  L  E  D  A  N  I  V  Q  P    1157

3541  TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT   3600
1158   L  G  L  T  I  L  G  K  H  L  Y  W  I  D  R  Q  Q  Q  M  I    1177

3601  CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA   3660
1178   E  R  V  E  K  T  T  G  D  K  R  T  R  I  Q  G  R  V  A  H    1197

3661  CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG   3720
1198   L  T  G  I  H  A  V  E  E  V  S  L  E  E  F  S  A  H  P  C    1217

3721  TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG   3780
1218   A  R  D  N  G  G  C  S  H  I  C  I  A  K  G  D  G  T  P  R    1237

3781  GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC   3840
1238   C  S  C  P  V  H  L  V  L  L  Q  N  L  L  T  C  G  E  P  P    1257
```

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FIG. 6H

```
3841  CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC  3900
1258   T  C  S  P  D  Q  F  A  C  A  T  G  E  I  D  C  I  P  G  A   1277

3901  CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT  3960
1278   W  R  C  D  G  F  P  E  C  D  D  Q  S  D  E  E  G  C  P  V   1297

3961  GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG  4020
1298   C  S  A  A  Q  F  P  C  A  R  G  Q  C  V  D  L  R  L  R  C   1317

4021  CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT  4080
1318   D  G  E  A  D  C  Q  D  R  S  D  E  V  D  C  D  A  I  C  L   1337

4081  GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC  4140
1338   P  N  Q  F  R  C  A  S  G  Q  C  V  L  I  K  Q  Q  C  D  S   1357

4141  CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC  4200
1358   F  P  D  C  I  D  G  S  D  E  L  M  C  E  I  T  K  P  P  S   1377

4201  AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT  4260
1378   D  D  S  P  A  H  S  S  A  I  G  P  V  I  G  I  I  L  S  L   1397

4261  CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG  4320
1398   F  V  M  G  G  V  Y  F  V  C  Q  R  V  V  C  Q  R  Y  A  G   1417

4321  GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT  4380
1418   A  N  G  P  F  P  H  E  Y  V  S  G  T  P  H  V  P  L  N  F   1437
```

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FIG. 6I

```
4381  CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT  4440
1438   I  A  P  G  G  S  Q  H  G  P  F  T  G  I  A  C  G  K  S  M   1457

4441  GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA  4500
1458   M  S  S  V  S  L  M  G  G  R  G  G  V  P  L  Y  D  R  N  H   1477

4501  CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT  4560
1478   V  T  G  A  S  S  S  S  S  S  S  T  K  A  T  L  Y  P  P  I   1497

4561  CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA  4620
1498   L  N  P  P  P  S  P  A  T  D  P  S  L  Y  N  M  D  M  F  Y   1517

4621  CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC  4680
1518   S  S  N  I  P  A  T  A  R  P  Y  R  P  Y  I  I  R  G  M  A   1537

4681  GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG  4740
1538   P  P  T  T  P  C  S  T  D  V  C  D  S  D  Y  S  A  S  R  W   1557

4741  GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC  4800
1558   K  A  S  K  Y  Y  L  D  L  N  S  D  S  D  P  Y  P  P  P  P   1577

4801  CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA  4860
1578   T  P  H  S  Q  Y  L  S  A  E  D  S  C  P  P  S  P  A  T  E   1597

4861  GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC  4920
1598   R  S  Y  F  H  L  F  P  P  P  P  S  P  C  T  D  S  S        1615
```

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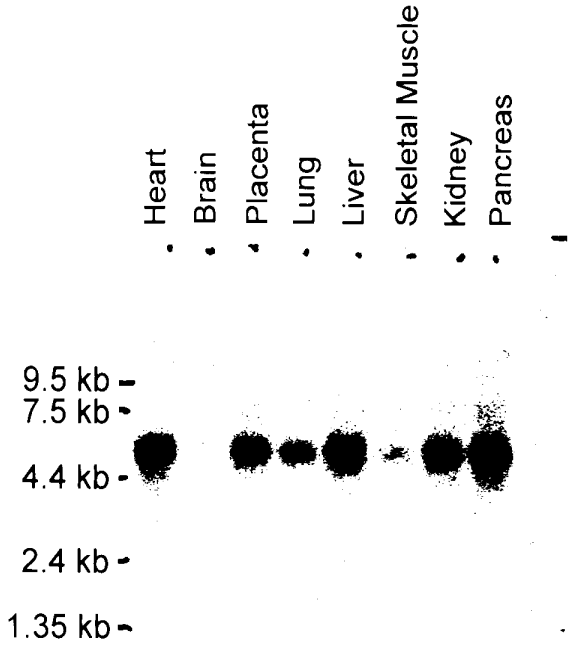
FIG. 6J

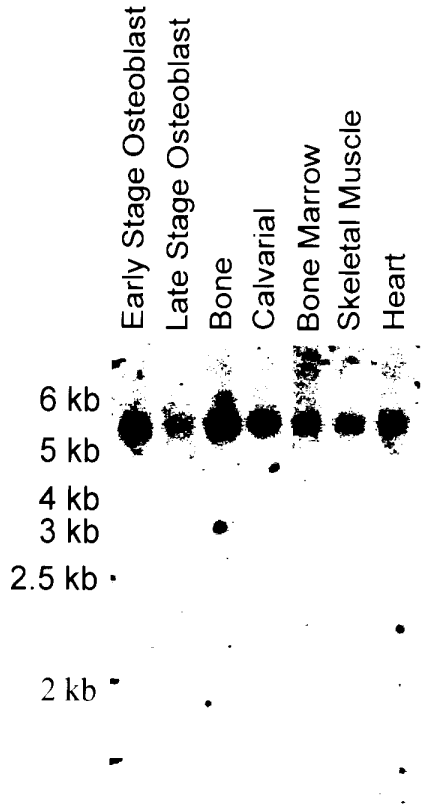
```
4921  TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA  4980
4981  AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA  5040
5041  TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT  5100
5101  AAACTTAATTTTGTAAAACA  5120
```

06/12/03
17224 U.S. PTO



Northern Blot Analysis - Zmax 1

FIG. 7A



Northern Blot Analysis - Zmax 1

FIG. 7B

06/12/03
17224 U.S. PTO

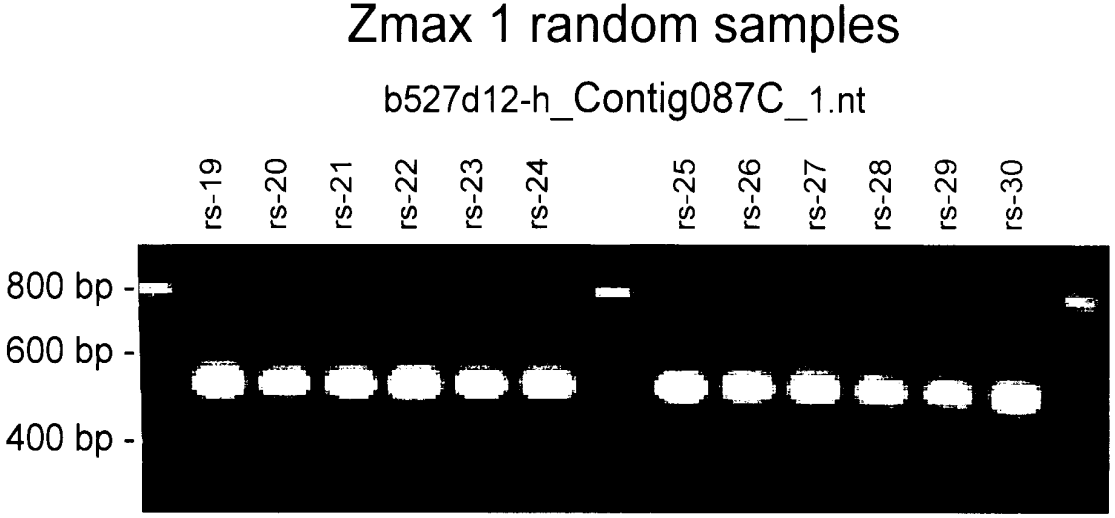


FIG. 8

06/12/03
17224 U.S. PTO

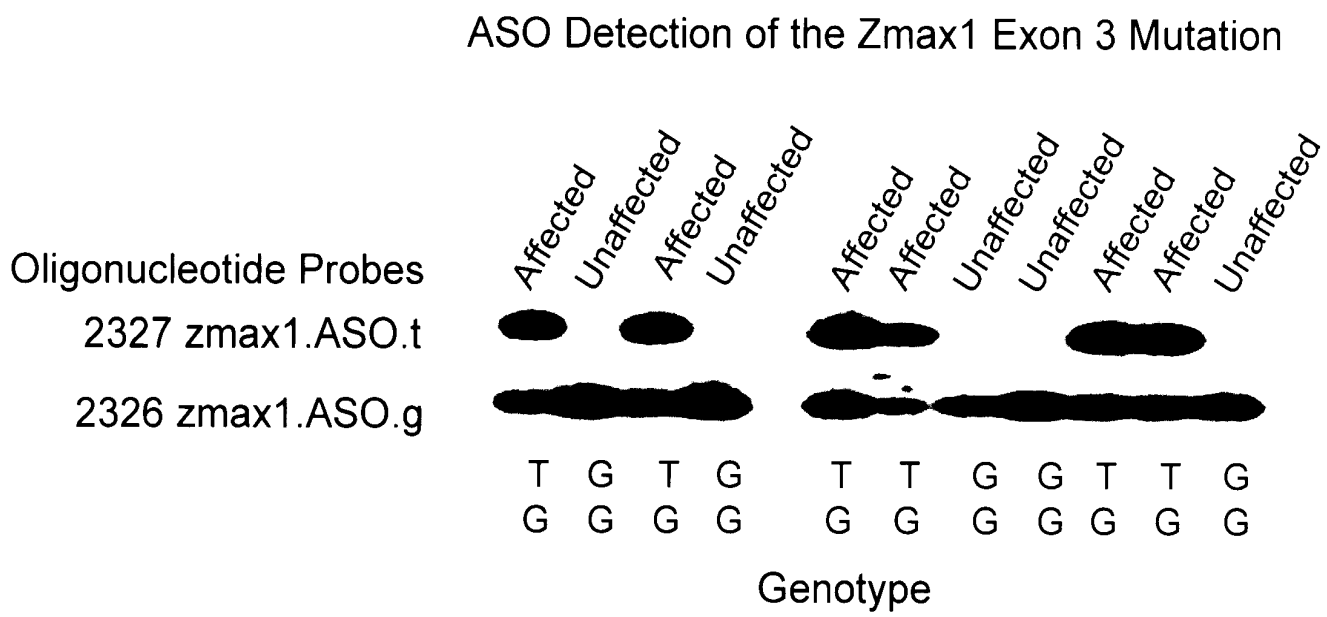


FIG. 9

17224 U.S. PTO
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Mouse Zmax1 In situ hybridization
100X Magnification

Antisense probe

FIG. 10A

Mouse Zmax1 In situ hybridization
100X Magnification

Sense probe

FIG. 10B

17224 U.S. PTO
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Mouse Zmax1 In situ hybridization
400X Magnification
Antisense probe

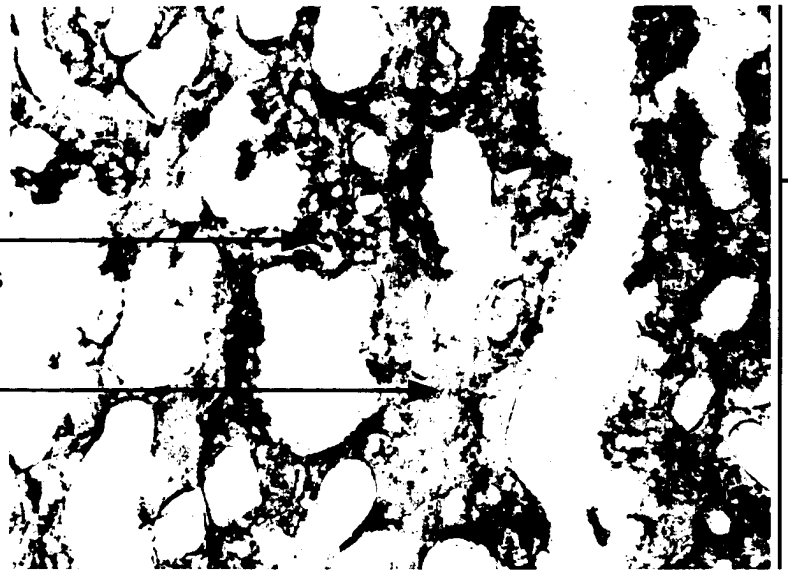


FIG. 11A

Mouse Zmax1 In situ hybridization
400X Magnification
Sense probe

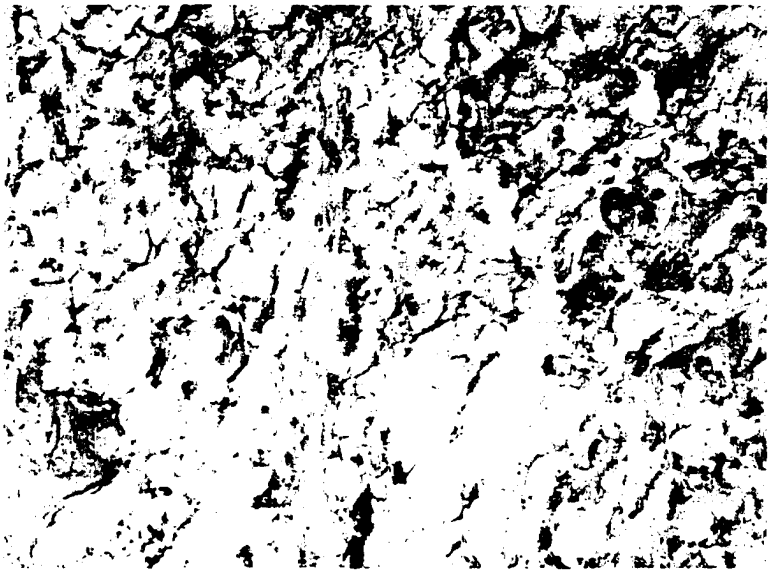


FIG. 11B

17224 U.S. PTO
06/12/03

Mouse Zmax1 In situ hybridization
400X Magnification
Antisense probe

FIG. 12A

Mouse Zmax1 In situ hybridization
400X Magnification
Sense probe

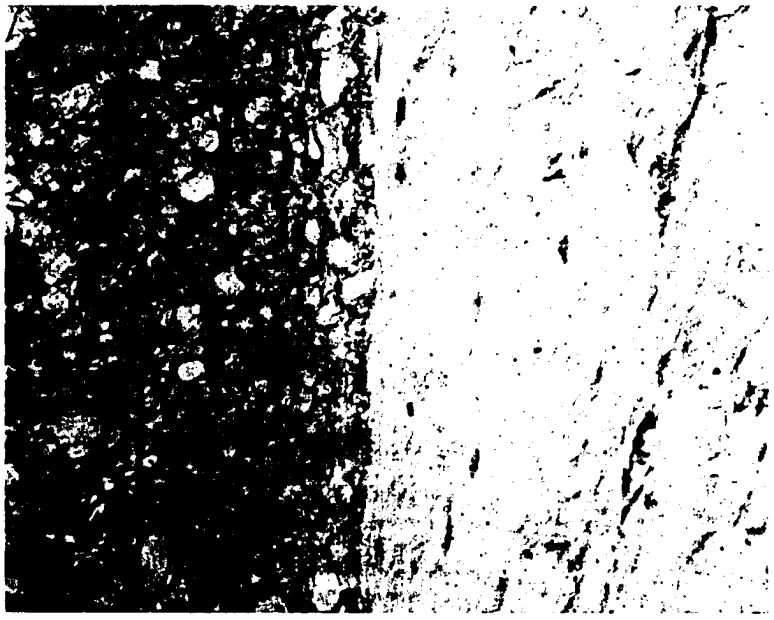
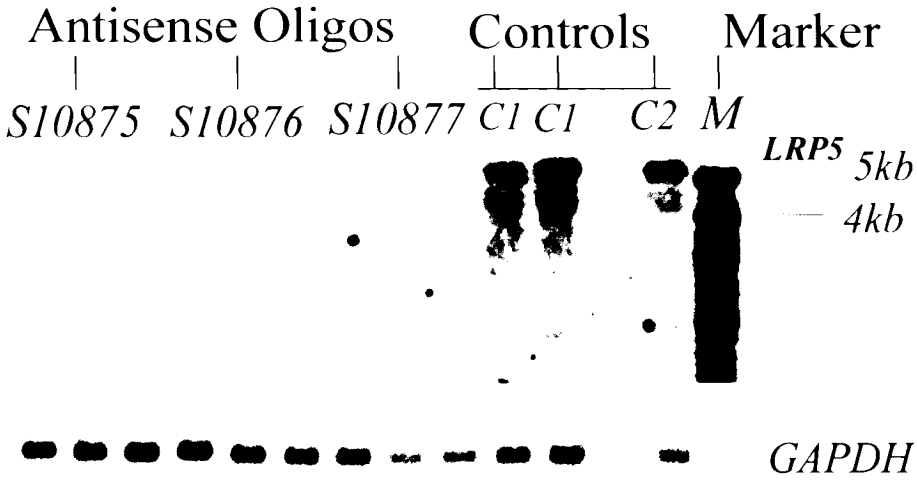


FIG. 12B

17224 U.S. PTO
06/12/03

Antisense Inhibition of Zmax1 Expression



MC-3T3 cells

FIG. 13